Amendments to the Claims:

1. (Currently Amended) A pair of primers for amplifying an hsp 65 (Heat Shock Protein 65) gene fragment of mycobacterial species, wherein one primer consists of the nucleotide sequence of SEQ ID NO: 55 and the other primer consists of the nucleotide sequence of SEQ ID NO: 56, and the size of the amplified hsp 65 gene fragment is 604 bp excluding the primers.

2. (Previously Presented) A polynucleotide of an hsp 65 gene fragment of mycobacterial species, wherein the fragment is amplified by using a pair of primers for amplifying the hsp 65 gene fragment of mycobacterial species, one primer consists of the nucleotide sequence of SEQ ID NO: 55 and the other primer consists of the nucleotide sequence of SEQ ID NO: 56; and the size of the amplified hsp 65 gene fragment is 604 bp excluding the primers.

3. (Previously Presented) A polynucleotide selected from the group of polynucleotides consisting of SEQ ID NO: 1 to SEQ ID NO: 54, and polynucleotides complementary thereto.

4. (Previously Presented) A polynucleotide set for the detection or identification of mycobacterial species wherein the set consists of at least two hsp 65 gene fragments selected from the group of polynucleotides consisting of SEQ ID NO: 1 to SEQ ID NO: 54 and polynucleotides complementary thereto.

5-7. Cancelled

8. (Previously Presented) A method for the identification of mycobacterial species comprising the steps of:

(1) amplifying an hsp 65 gene fragment of mycobacterial species with primers of claim 1, wherein the size of the amplified hsp 65 gene fragment is 644 bp including the primers; and

(2) analyzing the amplified fragment according to the RFLP (Restriction Fragment Length Polymorphism) analysis method using a restriction enzyme recognition site in the amplified fragment.

9. (Original) The method of claim 8, wherein the restriction enzyme is Xho I.

10. (Previously Presented) The method of claim 9 comprising the step of treating the amplified hsp 65 gene fragment with Xho I to produce restriction fragment(s), and analyzing the restriction fragment(s) according to an RFLP analysis method to differentiate TB complex (*Mycobacterium tuberculosis* complex) and MOTT (*Mycobacteria* other than *Mycobacterium tuberculosis*).

11. (Original) The method of claim 10, wherein the restriction fragments are 391-bp, 150-bp, and 103-bp fragments to identify the TB complex.

12. (Original) The method of claim 10, wherein the 644-bp hsp 65 gene fragment is not cleaved by a restriction enzyme to identify fast-growing mycobacteria of MOTT.

13. (Original) The method of claim 10, wherein the restriction fragments are 391-bp, 169-bp, and 48-bp to identify a mycobacterial species selected from the group consisting of *M, avium*, *M. intracellulare*, *M. celatum*, *M. shimoidei*, and *M. szulgai*.

14. (Original) The method of claim 10, wherein the restriction fragments are 391-bp and 253-bp to identify a mycobacterial species selected from the group consisting of *M, gastri*, *M. genavense, M. gordonae, M. haemophilum, M. kansasii, M. malmoense, M. marinum, M. scrofulaceum, M. simiae,* and *M. ulcerans*.

15. (Original) A kit for the differentiation or diagnosis of TB complex and MOTT comprising a pair of primers of claim 1 and Xho I, wherein the mycobacterial species is

differentiated or diagnosed based on the size of restriction fragment(s) which is obtained by amplifying an hsp 65 gene fragment of mycobacterial species in a sample with the primers to produce an amplified fragment and analyzing the amplified fragment according to an RFLP analysis method.

16. (Previously Presented) A method for the identification of a mycobacterial species comprising the steps of:

(1) amplifying an hsp 65 gene fragment of a mycobacterial species of interest with primers for amplifying an hsp65 gene of mycobacteria; and

(2) hybridizing the amplified hsp65 gene fragment with a probe set consisting of at least a probe selected from the group of polynucleotides consisting of SEQ ID NO: 1 to SEQ ID NO: 54 and polynucleotides complementary thereto.